Figure 1. Sequence of *C. pneumoniae* ATP-binding cassette gene

```
acttcccccc tgctaaacta tgctcagata atgctgctat gattgcaggt ctagggggag 60

aaaattttca aaaaaactct agtattccgg aaattcgtat atg cgc aag ata tca   115
                                            Met Arg Lys Ile Ser
                                             1               5

gtg gga atc tgt atc acc att ctc ctt agc ctc tcc gta gtc ctc caa   163
Val Gly Ile Cys Ile Thr Ile Leu Leu Ser Leu Ser Val Val Leu Gln
                10                  15                  20

ggc tgc aag gag tcc agt cac tcc tct aca tct cgg gga gaa ctc gct   211
Gly Cys Lys Glu Ser Ser His Ser Ser Thr Ser Arg Gly Glu Leu Ala
            25                  30                  35

att aat ata aga gat gaa ccc cgt tct tta gat cca aga caa gtg cga   259
Ile Asn Ile Arg Asp Glu Pro Arg Ser Leu Asp Pro Arg Gln Val Arg
        40                  45                  50

ctt ctt tca gaa atc agc ctt gtc aaa cat atc tat gag gga tta gtt   307
Leu Leu Ser Glu Ile Ser Leu Val Lys His Ile Tyr Glu Gly Leu Val
    55                  60                  65

caa gaa aat aat ctt tca gga aat ata gag cct gct ctt gca gaa gac   355
Gln Glu Asn Asn Leu Ser Gly Asn Ile Glu Pro Ala Leu Ala Glu Asp
70                  75                  80                  85

tac tct ctt tcc tcg gac gga ctc act tat act ttt aaa ctg aaa tca   403
Tyr Ser Leu Ser Ser Asp Gly Leu Thr Tyr Thr Phe Lys Leu Lys Ser
                90                  95                  100

gct ttt tgg agt aat ggc gac ccc tta aca gct gaa gac ttt ata gaa   451
Ala Phe Trp Ser Asn Gly Asp Pro Leu Thr Ala Glu Asp Phe Ile Glu
            105                 110                 115

tct tgg aaa caa gta gct act caa gaa gtc tca gga atc tat gct ttt   499
Ser Trp Lys Gln Val Ala Thr Gln Glu Val Ser Gly Ile Tyr Ala Phe
        120                 125                 130

gcc ttg aat cca att aaa aat gta cga aag atc caa gag gga cac ctc   547
Ala Leu Asn Pro Ile Lys Asn Val Arg Lys Ile Gln Glu Gly His Leu
    135                 140                 145

tcc ata gac cat ttt gga gtg cac tct cct aat gaa tct aca ctt gtt   595
Ser Ile Asp His Phe Gly Val His Ser Pro Asn Glu Ser Thr Leu Val
150                 155                 160                 165

gtt acc ctg gaa tcc cca acc tcg cat ttc tta aaa ctt tta gct ctt   643
Val Thr Leu Glu Ser Pro Thr Ser His Phe Leu Lys Leu Leu Ala Leu
                170                 175                 180
```

Figure 1 Cont.

```
cca gtc ttt ttc ccc gtt cat aaa tct caa aga acc ctg caa tcc aaa   691
Pro Val Phe Phe Pro Val His Lys Ser Gln Arg Thr Leu Gln Ser Lys
            185                 190                 195

tct cta cct ata gca agc gga gct ttc tat cct aaa aat atc aaa caa   739
Ser Leu Pro Ile Ala Ser Gly Ala Phe Tyr Pro Lys Asn Ile Lys Gln
        200                 205                 210

aaa caa tgg ata aaa ctc tca aaa aac cct cac tac tat aat caa agt   787
Lys Gln Trp Ile Lys Leu Ser Lys Asn Pro His Tyr Tyr Asn Gln Ser
    215                 220                 225

cag gtg gaa act aaa acg att acg att cac ttc att ccc gat gca aac   835
Gln Val Glu Thr Lys Thr Ile Thr Ile His Phe Ile Pro Asp Ala Asn
230                 235                 240                 245

aca gca gca aaa cta ttt aat cag gga aaa ctc aat tgg caa gga cct   883
Thr Ala Ala Lys Leu Phe Asn Gln Gly Lys Leu Asn Trp Gln Gly Pro
                250                 255                 260

cct tgg gga gaa cgc att cct caa gaa acc cta tcc aat tta cag tct   931
Pro Trp Gly Glu Arg Ile Pro Gln Glu Thr Leu Ser Asn Leu Gln Ser
            265                 270                 275

aag ggg cac tta cac tct ttt gat gtc gca gga acc tca tgg ctc acc   979
Lys Gly His Leu His Ser Phe Asp Val Ala Gly Thr Ser Trp Leu Thr
        280                 285                 290

ttc aat atc aat aaa ttc ccc ctc aac aat atg aag ctt aga gaa gcc   1027
Phe Asn Ile Asn Lys Phe Pro Leu Asn Asn Met Lys Leu Arg Glu Ala
    295                 300                 305

tta gca tca gcc tta gat aag gaa gct ctt gtc tca act ata ttc tta   1075
Leu Ala Ser Ala Leu Asp Lys Glu Ala Leu Val Ser Thr Ile Phe Leu
310                 315                 320                 325

ggc cgt gca aaa act gcc gat cat ctc cta cct aca aat att cat agc   1123
Gly Arg Ala Lys Thr Ala Asp His Leu Leu Pro Thr Asn Ile His Ser
                330                 335                 340

tat ccc gaa cat caa aaa caa gag atg gca caa cgc caa gct tac gct   1171
Tyr Pro Glu His Gln Lys Gln Glu Met Ala Gln Arg Gln Ala Tyr Ala
            345                 350                 355

aaa aaa ctc ttt aaa gaa gct tta gaa gaa ctc caa atc act gct aaa   1219
Lys Lys Leu Phe Lys Glu Ala Leu Glu Glu Leu Gln Ile Thr Ala Lys
        360                 365                 370

gat ctc gaa cat ctt aat ctt atc ttt ccc gtt tcc tcg tca gca agt   1267
Asp Leu Glu His Leu Asn Leu Ile Phe Pro Val Ser Ser Ser Ala Ser
    375                 380                 385
```

Figure 1 Cont.

```
tct tta cta gtc caa ctt ata cga gaa cag tgg aaa gaa agt tta ggg   1315
Ser Leu Leu Val Gln Leu Ile Arg Glu Gln Trp Lys Glu Ser Leu Gly
390                 395                 400                 405

ttc gct atc cct att gtc gga aag gaa ttt gct ctt ctc caa gca gac   1363
Phe Ala Ile Pro Ile Val Gly Lys Glu Phe Ala Leu Leu Gln Ala Asp
                410                 415                 420

cta tct tca ggg aac ttc tct tta gct aca gga gga tgg ttc gca gac   1411
Leu Ser Ser Gly Asn Phe Ser Leu Ala Thr Gly Gly Trp Phe Ala Asp
            425                 430                 435

ttt gct gat cct atg gca ttt cta acg atc ttt gct tat cca tca gga   1459
Phe Ala Asp Pro Met Ala Phe Leu Thr Ile Phe Ala Tyr Pro Ser Gly
        440                 445                 450

gtt cct cct tat gca atc aac cat aag gac ttc cta gaa att cta caa   1507
Val Pro Pro Tyr Ala Ile Asn His Lys Asp Phe Leu Glu Ile Leu Gln
    455                 460                 465

aac ata gaa caa gag caa gat cac caa aaa cgc tcg gaa tta gtg tcg   1555
Asn Ile Glu Gln Glu Gln Asp His Gln Lys Arg Ser Glu Leu Val Ser
470                 475                 480                 485

caa gct tct ctt tac cta gag acc ttt cat att att gag ccg atc tac   1603
Gln Ala Ser Leu Tyr Leu Glu Thr Phe His Ile Ile Glu Pro Ile Tyr
                490                 495                 500

cac gac gca ttt caa ttt gct atg aat aaa aaa ctt tct aat cta gga   1651
His Asp Ala Phe Gln Phe Ala Met Asn Lys Lys Leu Ser Asn Leu Gly
            505                 510                 515

gtc tca cca aca gga gtt gtg gac ttc cgt tat gct aag gaa aat       1696
Val Ser Pro Thr Gly Val Val Asp Phe Arg Tyr Ala Lys Glu Asn
        520                 525                 530

tagcacctct tttaatctcg caaacttgtc aagaactgaa tcttatacta aactgggtgc 1756

ctttgtggca cctcgtttcc ttctgactgc tcttctctct cta                   1799
```

Figure 2. Restriction enzyme analysis of the *C. pneumoniae* ATP-binding cassette gene

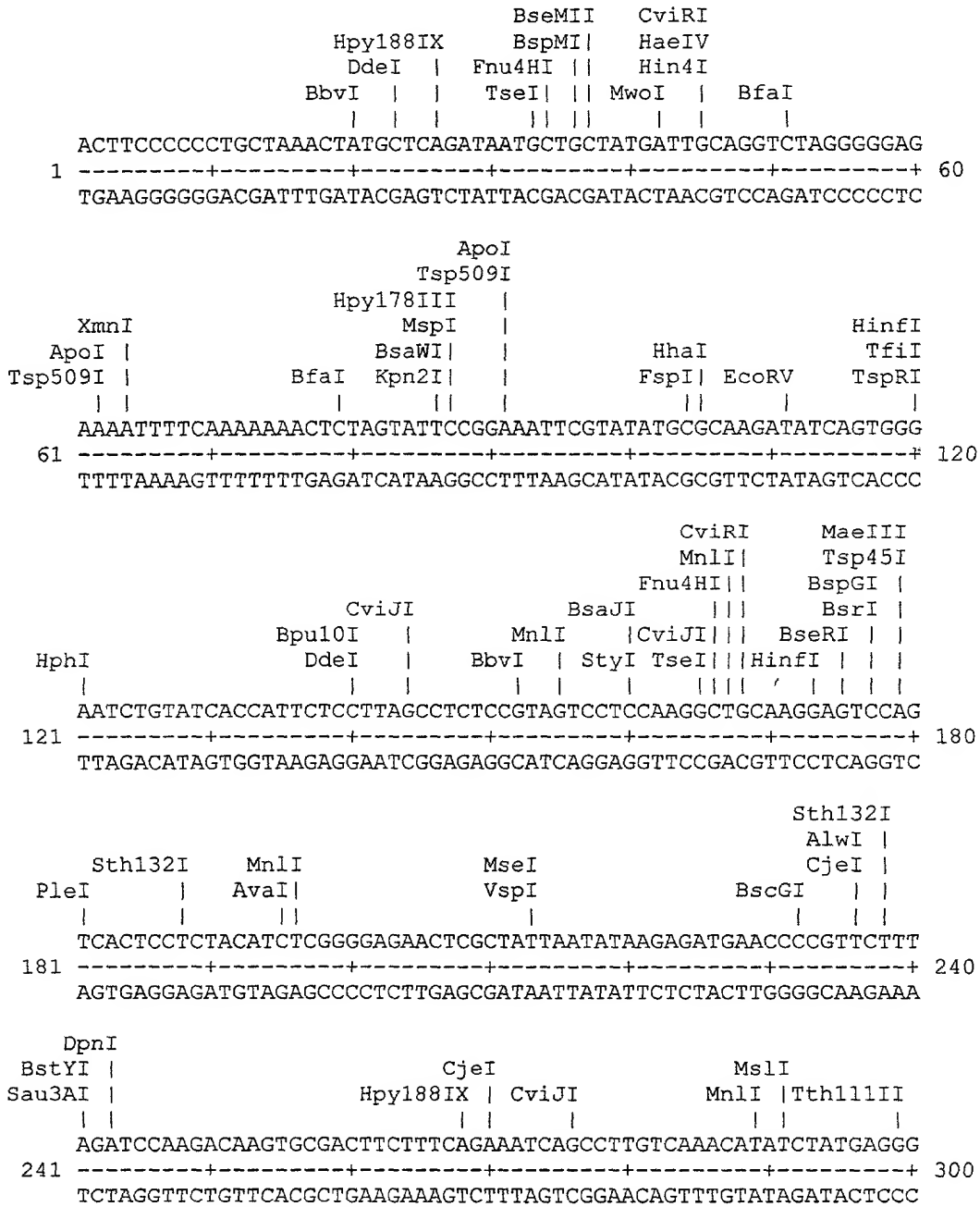

Figure 2 Cont.

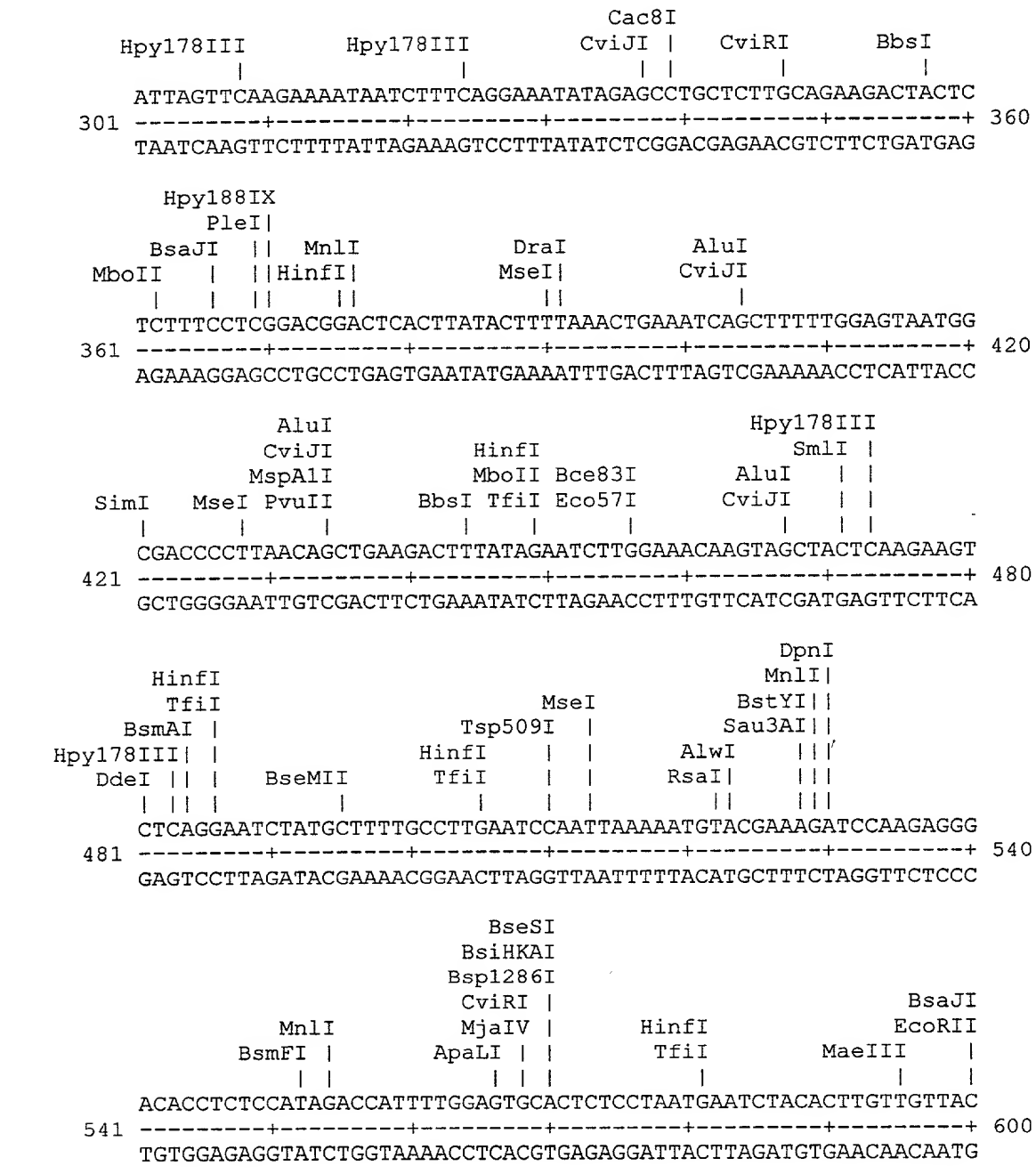

Figure 2 Cont.

```
                                        AluI
    HinfI                               CviJI   EarI
     TfiI                    MseI       CjePI |   SapI
 ScrFI  |                   MnlI| MboII    | |  BsrI|        BscGI
    |  |                      ||     |    | |     ||            |
    CCTGGAATCCCCAACCTCGCATTTCTTAAAACTTTTAGCTCTTCCAGTCTTTTTCCCCGT
601 ---------+---------+---------+---------+---------+---------+ 660
    GGACCTTAGGGGTTGGAGCGTAAAGAATTTTGAAAATCGAGAAGGTCAGAAAAAGGGGCA

                                                          AluI
                                                          CviJI
                                                        MwoI  |
                                                      AciI |  |
Sth132I CjePI        CviRI              SfcI  Cac8I | |  |  |
      |     |           |                  |      | | |  |  |
    TCATAAATCTCAAAGAACCCTGCAATCCAAATCTCTACCTATAGCAAGCGGAGCTTTCTA
661 ---------+---------+---------+---------+---------+---------+ 720
    AGTATTTAGAGTTTCTTGGGACGTTAGGTTTAGAGATGGATATCGTTCGCCTCGAAAGAT

                          Tth111II                          MnlI
                             |                               |
    TCCTAAAAATATCAAACAAAAACAATGGATAAAACTCTCAAAAAACCCTCACTACTATAA
721 ---------+---------+---------+---------+---------+---------+ 780
    AGGATTTTTATAGTTTGTTTTTGTTACCTATTTTGAGAGTTTTTTGGGAGTGATGATATT

                                                 Sth132I   Fnu4HI
                                HinfI    Hpy178III      |    TseI|
                                 TfiI SfaNI      | CviRI| MwoI  ||
                                   |     |       |     ||    |  ||
    TCAAAGTCAGGTGGAAACTAAAACGATTACGATTCACTTCATTCCCGATGCAAACACAGC
781 ---------+---------+---------+---------+---------+---------+ 840
    AGTTTCAGTCCACCTTTGATTTTGCTAATGCTAAGTGAAGTAAGGGCTACGTTTGTGTCG

                                      AvaII         MnlI
                                    EcoO109I    Bce83I  |
            MseI                      Psp5II     BslI|  |
           BbvI|            MunI     Sau96I BsaJI  ||  |  BsmI
   Tth111II   ||          Tsp509I  Sse8647I  StyI  ||  |  XmnI
         |    ||            |         |      |   ||  |     |
    AGCAAAACTATTTAATCAGGGAAAACTCAATTGGCAAGGACCTCCTTGGGGAGAACGCAT
841 ---------+---------+---------+---------+---------+---------+ 900
    TCGTTTTGATAAATTAGTCCCTTTTGAGTTAACCGTTCCTGGAGGAACCCCTCTTGCGTA

                                      BseSI
Hpy178III       Tsp509I       DdeI Bsp1286I
   SmlI |   MnlI      |  Bst4CI  |    BmgI |
      | |      |      |       |  |      | |
    TCCTCAAGAAACCCTATCCAATTTACAGTCTAAGGGGCACTTACACTCTTTTGATGTCGC
901 ---------+---------+---------+---------+---------+---------+ 960
    AGGAGTTCTTTGGGATAGGTTAAATGTCAGATTCCCCGTGAATGTGAGAAAACTACAGCG
```

Figure 2 Cont.

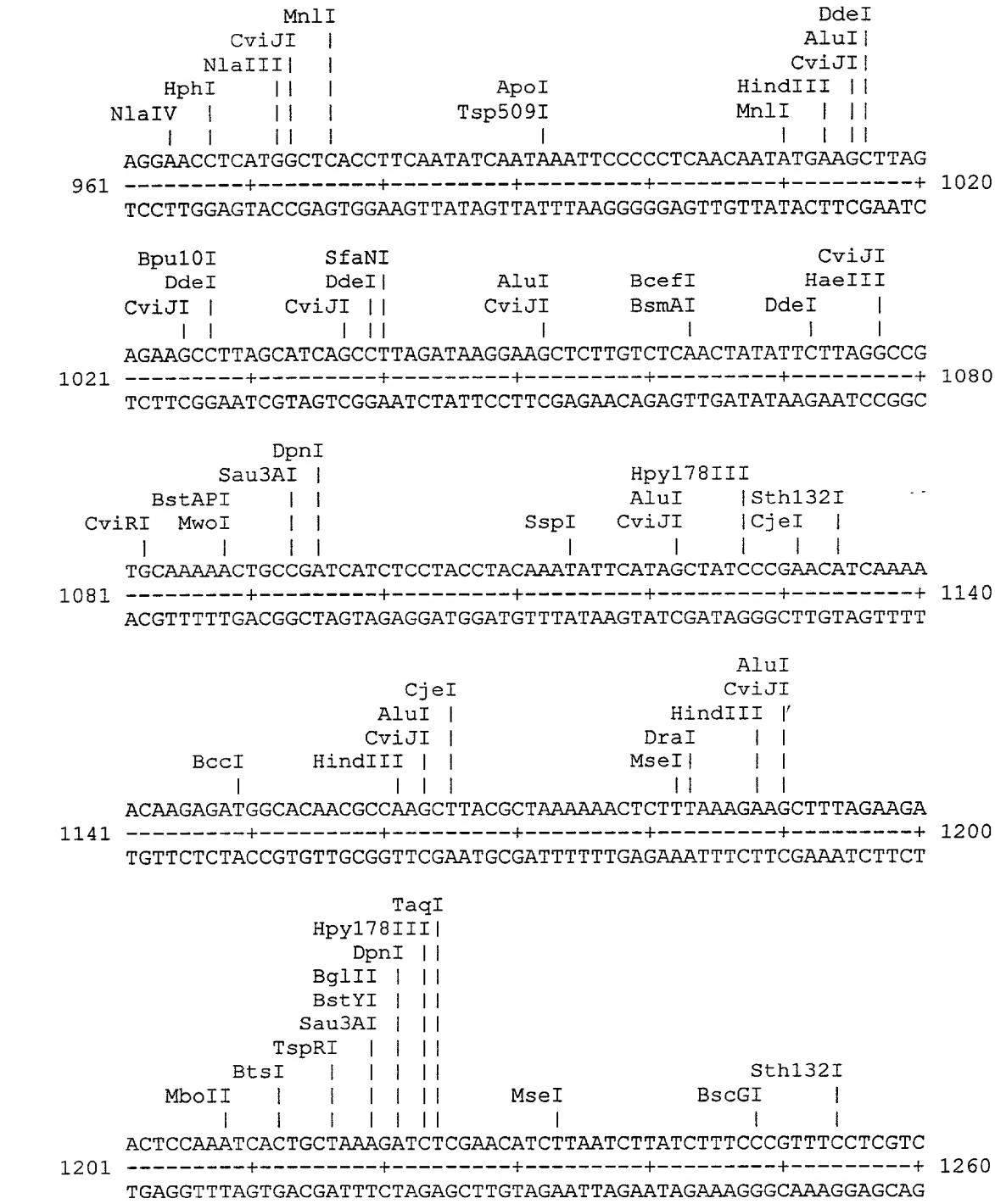

Figure 2 Cont.

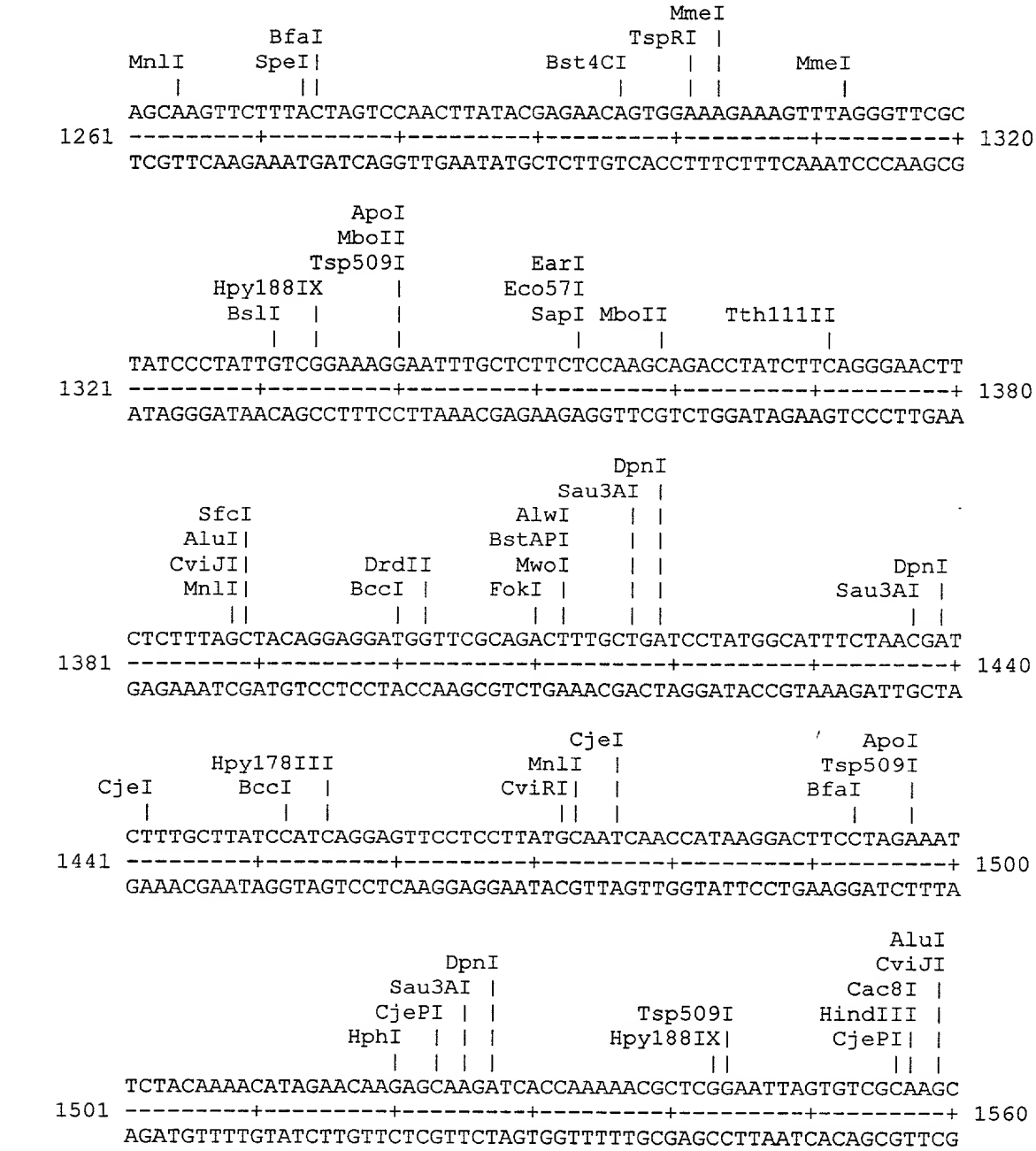

Figure 2 Cont.

```
                BfaI                                DpnI
             BsaI  |                             Sau3AI |                HgaI
            BsmAI  |                            CviJI | |             Tsp509I
                |  |                                  | | |                |
          TTCTCTTTACCTAGAGACCTTTCATATTATTGAGCCGATCTACCACGACGCATTTCAATT
     1561 ---------+---------+---------+---------+---------+---------+ 1620
          AAGAGAAATGGATCTCTGGAAAGTATAATAACTCGGCTAGATGGTGCTGCGTAAAGTTAA

                                HinfI
                                CjeI|
                               HphI ||    PleI
                              BfaI| ||  BsmAI|          MjaIV
                                 || ||      ||            |
          TGCTATGAATAAAAAACTTTCTAATCTAGGAGTCTCACCAACAGGAGTTGTGGACTTCCG
     1621 ---------+---------+---------+---------+---------+---------+ 1680
          ACGATACTTATTTTTTGAAAGATTAGATCCTCAGAGTGGTTGTCCTCAACACCTGAAGGC

          Bpu10I
            DdeI                          MnlI                    HinfI
         CjeI  |Tsp509I              MseI    |      Hpy178III     TfiI TaqII
            |  |      |                 |    |              |       |     |
          TTATGCTAAGGAAAATTAGCACCTCTTTTAATCTCGCAAACTTGTCAAGAACTGAATCTT
     1681 ---------+---------+---------+---------+---------+---------+ 1740
          AATACGATTCCTTTTAATCGTGGAGAAAATTAGAGCGTTTGAACAGTTCTTGACTTAGAA

                   NlaIV      NlaIV
                   BsrI|      BanI |        Hpy188IX
                  BanI||    BglI | |          MboII|         EarI
                BmrI |||    MwoI | |          MnlI ||         SapI
                   | |||       | | |             | ||          ' |
          ATACTAAACTGGGTGCCTTTGTGGCACCTCGTTTCCTTCTGACTGCTCTTCTCTCTCTA
     1741 ---------+---------+---------+---------+---------+--------- 1799
          TATGATTTGACCCACGGAAACACCGTGGAGCAAAGGAAGACTGACGAGAAGAGAGAGAT
```

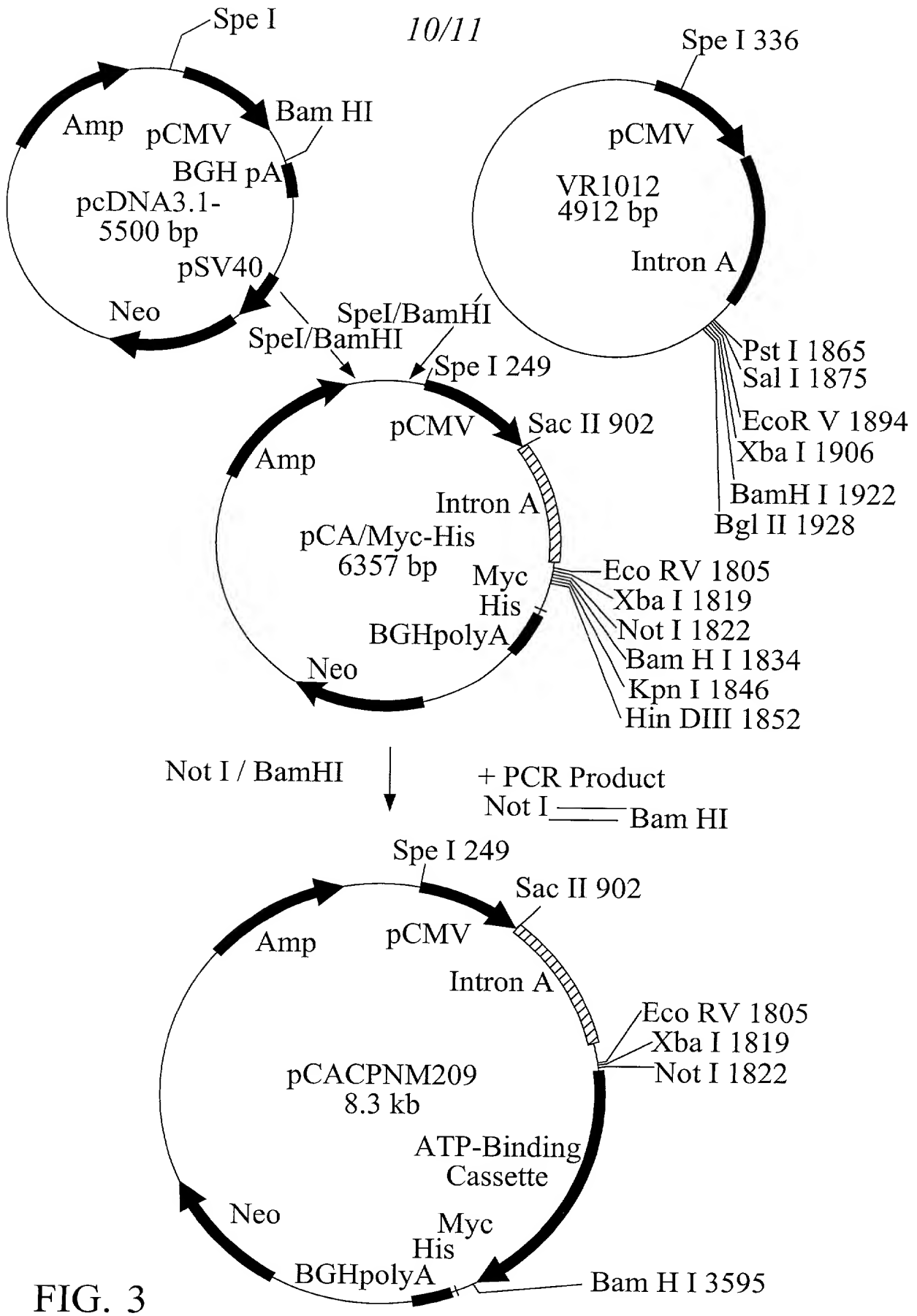

FIG. 3
Construction of pCACPNM209

Figure 4: Protective efficacy of DNA immunization with pCACPNM209